

### Amendments to the Specification:

Amend the paragraph beginning at page 12, line 13, of the specification as follows.

**Figure 3** is **Figures 3-1 to 3-3** are the amino acid sequence of *age-1* (SEQ ID NO: 1), as determined by sequencing cDNA clones, amplified reverse transcribed PCR fragments, and genomic regions described in Figure 1. PCR generated templates were sequenced without subcloning and verified by sequencing multiple isolates. *age-1* alleles were sequenced by PCR amplifying genomic regions and direct sequencing of templates without subcloning. Each mutation detected was verified by sequencing an independently amplified template. The AGE-1 sequence comparisons are to mouse p110 $\alpha$  (accession number P42337) (SEQ ID NO: 10), human p110 $\beta$  (accession number P42338) (SEQ ID NO: 11), and human p110 $\gamma$  (accession number P48736) (SEQ ID NO: 12). Regions highlighted in gray and black were picked out by Prettybox, aligned by the Pileup program as having extended regions of high amino acid similarity (Program Manual for the Wisconsin Package, Version 8, September 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711). Invariant amino acids in 3 of the 4 sequences are shown as black boxes. Similar amino acids in regions highlighted by 3 of 4 exact matches are highlighted in gray boxes. Allele lesions are shown above the amino

acid which was altered. The asterisks (\*) indicate a change to a stop codon. The brackets around *age-1(mg55)* show the region to which we mapped the *age-1(mg55)* breakpoint.

Amend the paragraph beginning at page 13, line 7, of the specification as follows.

~~Figure 4 is~~ Figures 4-1 and 4-2 are the nucleic acid sequence of an *age-1* cDNA (SEQ ID NO: 2).